

## SEQUENCE LISTING

<110> Whitehead Institute for Biomedical Research  
Hug, Christopher  
Lodish, Harvey F.

<120> USE OF T-CADHERIN AS A TARGET

<130> SER-100X

<150> US 60/526,956

<151> 2003-12-03

<160> 18

<170> PatentIn version 3.1

<210> 1

<211> 713

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> (1)..(22)

<223>

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<221> LIPID

<222> (693)..(693)

<223> GPI-ANCHOR

<220>

<221> PROPEP

<222> (23)..(139)

<223>

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<221> PROPEP

<222> (694)..(713)

<223>

<400> 1

Met Gln Pro Arg Thr Pro Leu Val Leu Cys Val Leu Leu Ser Gln Val  
1 5 10 15

Leu Leu Leu Thr Ser Ala Glu Asp Leu Asp Cys Thr Pro Gly Phe Gln  
20 25 30

Gln Lys Val Phe His Ile Asn Gln Pro Ala Glu Phe Ile Glu Asp Gln  
35 40 45

Ser Ile Leu Asn Leu Thr Phe Ser Asp Cys Lys Gly Asn Asp Lys Leu  
50 55 60

Arg Tyr Glu Val Ser Ser Pro Tyr Phe Lys Val Asn Ser Asp Gly Gly

65

70

75

80

Leu Val Ala Leu Arg Asn Ile Thr Ala Val Gly Lys Thr Leu Phe Val  
 85 90 95

His Ala Arg Thr Pro His Ala Glu Asp Met Ala Glu Leu Val Ile Val  
 100 105 110

Gly Gly Lys Asp Ile Gln Gly Ser Leu Gln Asp Ile Phe Lys Phe Ala  
 115 120 125

Arg Thr Ser Pro Val Pro Arg Gln Lys Arg Ser Ile Val Val Ser Pro  
 130 135 140

Ile Leu Ile Pro Glu Asn Gln Arg Gln Pro Phe Pro Arg Asp Val Gly  
 145 150 155 160

Lys Val Val Asp Ser Asp Arg Pro Glu Arg Ser Lys Phe Arg Leu Thr  
 165 170 175

Gly Lys Gly Val Asp Gln Glu Pro Lys Gly Ile Phe Arg Ile Asn Glu  
 180 185 190

Asn Thr Gly Ser Val Ser Val Thr Arg Thr Leu Asp Arg Glu Val Ile  
 195 200 205

Ala Val Tyr Gln Leu Phe Val Glu Thr Thr Asp Val Asn Gly Lys Thr  
 210 215 220

Leu Glu Gly Pro Val Pro Leu Glu Val Ile Val Ile Asp Gln Asn Asp  
 225 230 235 240

Asn Arg Pro Ile Phe Arg Glu Gly Pro Tyr Ile Gly His Val Met Glu  
 245 250 255

Gly Ser Pro Thr Gly Thr Thr Val Met Arg Met Thr Ala Phe Asp Ala  
 260 265 270

Asp Asp Pro Ala Thr Asp Asn Ala Leu Leu Arg Tyr Asn Ile Arg Gln  
 275 280 285

Gln Thr Pro Asp Lys Pro Ser Pro Asn Met Phe Tyr Ile Asp Pro Glu  
 290 295 300

Lys Gly Asp Ile Val Thr Val Val Ser Pro Ala Leu Leu Asp Arg Glu  
 305 310 315 320

Thr Leu Glu Asn Pro Lys Tyr Glu Leu Ile Ile Glu Ala Gln Asp Met  
 325 330 335

Ala Gly Leu Asp Val Gly Leu Thr Gly Thr Ala Thr Ala Thr Ile Met  
 340 345 350

Ile Asp Asp Lys Asn Asp His Ser Pro Lys Phe Thr Lys Lys Glu Phe  
 355 360 365

Gln Ala Thr Val Glu Glu Gly Ala Val Gly Val Ile Val Asn Leu Thr  
 370 375 380

Val Glu Asp Lys Asp Asp Pro Thr Thr Gly Ala Trp Arg Ala Ala Tyr  
 385 390 395 400  
 Thr Ile Ile Asn Gly Asn Pro Gly Gln Ser Phe Glu Ile His Thr Asn  
 405 410 415  
 Pro Gln Thr Asn Glu Gly Met Leu Ser Val Val Lys Pro Leu Asp Tyr  
 420 425 430  
 Glu Ile Ser Ala Phe His Thr Leu Leu Ile Lys Val Glu Asn Glu Asp  
 435 440 445  
 Pro Leu Val Pro Asp Val Ser Tyr Gly Pro Ser Ser Thr Ala Thr Val  
 450 455 460  
 His Ile Thr Val Leu Asp Val Asn Glu Gly Pro Val Phe Tyr Pro Asp  
 465 470 475 480  
 Pro Met Met Val Thr Arg Gln Glu Asp Leu Ser Val Gly Ser Val Leu  
 485 490 495  
 Leu Thr Val Asn Ala Thr Asp Pro Asp Ser Leu Gln His Gln Thr Ile  
 500 505 510  
 Arg Tyr Ser Val Tyr Lys Asp Pro Ala Gly Trp Leu Asn Ile Asn Pro  
 515 520 525  
 Ile Asn Gly Thr Val Asp Thr Thr Ala Val Leu Asp Arg Glu Ser Pro  
 530 535 540  
 Phe Val Asp Asn Ser Val Tyr Thr Ala Leu Phe Leu Ala Ile Asp Ser  
 545 550 555 560  
 Gly Asn Pro Pro Ala Thr Gly Thr Gly Thr Leu Leu Ile Thr Leu Glu  
 565 570 575  
 Asp Val Asn Asp Asn Ala Pro Phe Ile Tyr Pro Thr Val Ala Glu Val  
 580 585 590  
 Cys Asp Asp Ala Lys Asn Leu Ser Val Val Ile Leu Gly Ala Ser Asp  
 595 600 605  
 Lys Asp Leu His Pro Asn Thr Asp Pro Phe Lys Phe Glu Ile His Lys  
 610 615 620  
 Gln Ala Val Pro Asp Lys Val Trp Lys Ile Ser Lys Ile Asn Asn Thr  
 625 630 635 640  
 His Ala Leu Val Ser Leu Leu Gln Asn Leu Asn Lys Ala Asn Tyr Asn  
 645 650 655  
 Leu Pro Ile Met Val Thr Asp Ser Gly Lys Pro Pro Met Thr Asn Ile  
 660 665 670  
 Thr Asp Leu Arg Val Gln Val Cys Ser Cys Arg Asn Ser Lys Val Asp  
 675 680 685

Cys Asn Ala Ala Gly Ala Leu Arg Phe Ser Leu Pro Ser Val Leu Leu  
 690 695 700

Leu Ser Leu Phe Ser Leu Ala Cys Leu  
 705 710

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 <213> Homo sapiens

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 <222> (42)..(107)  
 <223> Collagen-like domain

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 <222> (108)..(244)  
 <223> C1q domain

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Met Leu Leu Leu Gly Ala Val Leu Leu Leu Ala Leu Pro Gly His  
 1 5 10 15

Asp Gln Glu Thr Thr Gln Gly Pro Gly Val Leu Leu Pro Leu Pro  
 20 25 30

Lys Gly Ala Cys Thr Gly Trp Met Ala Gly Ile Pro Gly His Pro Gly  
 35 40 45

His Asn Gly Ala Pro Gly Arg Asp Gly Arg Asp Gly Thr Pro Gly Glu  
 50 55 60

Lys Gly Glu Lys Gly Asp Pro Gly Leu Ile Gly Pro Lys Gly Asp Ile  
 65 70 75 80

Gly Glu Thr Gly Val Pro Gly Ala Glu Gly Pro Arg Gly Phe Pro Gly  
 85 90 95

Ile Gln Gly Arg Lys Gly Glu Pro Gly Glu Gly Ala Tyr Val Tyr Arg  
 100 105 110

Ser Ala Phe Ser Val Gly Leu Glu Thr Tyr Val Thr Ile Pro Asn Met  
 115 120 125

Pro Ile Arg Phe Thr Lys Ile Phe Tyr Asn Gln Gln Asn His Tyr Asp  
 130 135 140

Gly Ser Thr Gly Lys Phe His Cys Asn Ile Pro Gly Leu Tyr Tyr Phe

145	150	155	160
Ala Tyr His Ile Thr Val Tyr Met Lys Asp Val Lys Val Ser Leu Phe			
165	170	175	
Lys Lys Asp Lys Ala Met Leu Phe Thr Tyr Asp Gln Tyr Gln Glu Asn			
180	185	190	
Asn Val Asp Gln Ala Ser Gly Ser Val Leu Leu His Leu Glu Val Gly			
195	200	205	
Asp Gln Val Trp Leu Gln Val Tyr Gly Glu Gly Glu Arg Asn Gly Leu			
210	215	220	
Tyr Ala Asp Asn Asp Asn Asp Ser Thr Phe Thr Gly Phe Leu Leu Tyr			
225	230	235	240
His Asp Thr Asn			

<210> 3  
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 <212> PRT  
 <213> Mus musculus

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 <222> (45)..(110)  
 <223> Collagen-like domain

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 <222> (111)..(247)  
 <223> C1q domain

<400> 3

Met Leu Leu Leu Gln Ala Leu Leu Phe Leu Leu Ile Leu Pro Ser His  
 1 5 10 15

Ala Glu Asp Asp Val Thr Thr Glu Glu Leu Ala Pro Ala Leu Val  
 20 25 30

Pro Pro Pro Lys Gly Thr Cys Ala Gly Trp Met Ala Gly Ile Pro Gly  
 35 40 45

His Pro Gly His Asn Gly Thr Pro Gly Arg Asp Gly Arg Asp Gly Thr  
 50 55 60

Pro Gly Glu Lys Gly Glu Lys Gly Asp Ala Gly Leu Leu Gly Pro Lys  
 65 70 75 80

Gly Glu Thr Gly Asp Val Gly Met Thr Gly Ala Glu Gly Pro Arg Gly  
 85 90 95

Phe Pro Gly Thr Pro Gly Arg Lys Gly Glu Pro Gly Glu Ala Ala Tyr  
100 105 110

Met Tyr Arg Ser Ala Phe Ser Val Gly Leu Glu Thr Arg Val Thr Val  
115 120 125

Pro Asn Val Pro Ile Arg Phe Thr Lys Ile Phe Tyr Asn Gln Gln Asn  
130 135 140

His Tyr Asp Gly Ser Thr Gly Lys Phe Tyr Cys Asn Ile Pro Gly Leu  
145 150 155 160

Tyr Tyr Phe Ser Tyr His Ile Thr Val Tyr Met Lys Asp Val Lys Val  
165 170 175

Ser Leu Phe Lys Lys Asp Lys Ala Val Leu Phe Thr Tyr Asp Gln Tyr  
180 185 190

Gln Glu Lys Asn Val Asp Gln Ala Ser Gly Ser Val Leu Leu His Leu  
195 200 205

Glu Val Gly Asp Gln Val Trp Leu Gln Val Tyr Gly Asp Gly Asp His  
210 215 220

Asn Gly Leu Tyr Ala Asp Asn Val Asn Asp Ser Thr Phe Thr Gly Phe  
225 230 235 240

Leu Leu Tyr His Asp Thr Asn  
245

<210> 4  
<211> 714  
<212> PRT  
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<222> (1)..(22)  
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<223> GPI-ANCHOR

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<222> (694)..(714)  
<223>

<400> 4

Met Gln Pro Arg Thr Pro Leu Thr Leu Cys Val Leu Leu Ser Gln Val  
 1 5 10 15

Leu Leu Val Thr Ser Ala Asp Asp Leu Glu Cys Thr Pro Gly Phe Gln  
 20 25 30

Arg Lys Val Leu His Ile His Gln Pro Ala Glu Phe Ile Glu Asp Gln  
 35 40 45

Pro Val Leu Asn Leu Thr Phe Asn Asp Cys Lys Gly Asn Glu Lys Leu  
 50 55 60

His Tyr Glu Val Ser Ser Pro His Phe Lys Val Asn Ser Asp Gly Thr  
 65 70 75 80

Leu Val Ala Leu Arg Asn Ile Thr Ala Val Gly Arg Thr Leu Phe Val  
 85 90 95

His Ala Arg Thr Pro His Ala Glu Asp Met Ala Glu Leu Val Ile Val  
 100 105 110

Gly Gly Lys Asp Ile Gln Gly Ser Leu Gln Asp Ile Phe Lys Phe Ala  
 115 120 125

Arg Thr Ser Pro Val Pro Arg Gln Lys Arg Ser Ile Val Val Ser Pro  
 130 135 140

Ile Leu Ile Pro Glu Asn Gln Arg Gln Pro Phe Pro Arg Asp Val Gly  
 145 150 155 160

Lys Val Val Asp Ser Asp Arg Pro Glu Gly Ser Lys Phe Arg Leu Thr  
 165 170 175

Gly Lys Gly Val Asp Gln Asp Pro Lys Gly Thr Phe Arg Ile Asn Glu  
 180 185 190

Asn Thr Gly Ser Val Ser Val Thr Arg Thr Leu Asp Arg Glu Thr Ile  
 195 200 205

Ala Thr Tyr Gln Leu Tyr Val Glu Thr Thr Asp Ala Ser Gly Lys Thr  
 210 215 220

Leu Glu Gly Pro Val Pro Leu Glu Val Ile Val Ile Asp Gln Asn Asp  
 225 230 235 240

Asn Arg Pro Ile Phe Arg Glu Gly Pro Tyr Ile Gly His Val Met Glu  
 245 250 255

Gly Ser Pro Thr Gly Thr Thr Val Met Arg Met Thr Ala Phe Asp Ala  
 260 265 270

Asp Asp Pro Ala Thr Asp Asn Ala Leu Trp Arg Tyr Asn Ile Arg Gln  
 275 280 285

Gln Thr Pro Asp Lys Pro Ser Pro Asn Met Phe Tyr Ile Asp Pro Glu  
 290 295 300

Lys Gly Asp Ile Val Thr Val Val Ser Pro Ala Leu Leu Asp Arg Glu

305	310	315	320
Thr Leu Glu Asn Pro Lys Tyr Glu Leu Ile Ile Glu Ala Gln Asp Met			
325	330	335	
Ala Gly Leu Asp Val Gly Leu Thr Gly Thr Ala Thr Ala Thr Ile Val			
340	345	350	
Ile Asp Asp Lys Asn Asp His Ser Pro Lys Phe Thr Lys Lys Glu Phe			
355	360	365	
Gln Ala Arg Val Glu Glu Gly Ala Val Gly Val Ile Val Asn Leu Thr			
370	375	380	
Val Glu Asp Lys Asp Asp Pro Thr Thr Gly Ala Trp Arg Ala Ala Tyr			
385	390	395	400
Thr Ile Ile Asn Gly Asn Pro Gly Gln Ser Phe Glu Ile His Thr Asn			
405	410	415	
Pro Gln Thr Asn Glu Gly Met Leu Ser Val Val Lys Pro Leu Asp Tyr			
420	425	430	
Glu Ile Ser Ala Phe His Thr Leu Leu Ile Lys Val Glu Asn Glu Asp			
435	440	445	
Pro Leu Val Pro Asp Val Ser Tyr Gly Pro Ser Ser Thr Ala Thr Val			
450	455	460	
His Ile Thr Val Leu Asp Val Asn Glu Gly Pro Val Phe Tyr Pro Asp			
465	470	475	480
Pro Met Met Val Thr Lys Gln Glu Asn Ile Ser Val Gly Ser Val Leu			
485	490	495	
Leu Thr Val Asn Ala Thr Asp Pro Asp Ser Leu Gln His Gln Thr Ile			
500	505	510	
Arg Tyr Ser Ile Tyr Lys Asp Pro Ala Gly Trp Leu Ser Ile Asn Pro			
515	520	525	
Ile Asn Gly Thr Val Asp Thr Thr Ala Val Leu Asp Arg Glu Ser Pro			
530	535	540	
Phe Val His Asn Ser Val Tyr Thr Ala Leu Phe Leu Ala Ile Asp Ser			
545	550	555	560
Gly Asn Pro Pro Ala Thr Gly Thr Gly Thr Leu Leu Ile Thr Leu Glu			
565	570	575	
Asp Ile Asn Asp Asn Ala Pro Val Ile Tyr Pro Thr Val Ala Glu Val			
580	585	590	
Cys Asp Asp Ala Arg Asn Leu Ser Val Val Ile Leu Gly Ala Ser Asp			
595	600	605	
Lys Asp Leu His Pro Asn Thr Asp Pro Phe Lys Phe Glu Ile His Lys			
610	615	620	

Gln Thr Val Pro Asp Lys Val Trp Lys Ile Ser Lys Ile Asn Asn Thr  
 625 630 635 640

His Ala Leu Val Ser Leu Leu Gln Asn Leu Asn Lys Ala Asn Tyr Asn  
 645 650 655

Leu Pro Ile Met Val Thr Asp Ser Gly Lys Pro Pro Met Thr Asn Ile  
 660 665 670

Thr Asp Leu Lys Val Gln Val Cys Ser Cys Lys Asn Ser Lys Val Asp  
 675 680 685

Cys Asn Gly Ala Gly Ala Leu His Leu Ser Leu Ser Leu Leu Leu Leu  
 690 695 700

Phe Ser Leu Leu Ser Leu Leu Ser Gly Leu  
 705 710

<210> 5

<211> 36

<212> DNA

<213> Artificial

<220>

<223> primer

<400> 5

aagaattccg ccaccatgct actgttgcaa gctctc

36

<210> 6

<211> 45

<212> DNA

<213> Artificial

<220>

<223> primer

<400> 6

gactacaagg acgacgatga caaggaagat gacgttacta caact

45

<210> 7

<211> 45

<212> DNA

<213> Artificial

<220>

<223> primer

<400> 7

cttgtcatcg tcgtccttgt agtcggcatg actggcagg attaa

45

<210> 8

<211> 30

<212> DNA

<213> Artificial

<220>

<223> primer

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tttgaattct cagttggat catggtagag 30

<210> 9  
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<220>

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<400> 9  
aagaattccg ccaccatgct actgttgcaa gctctc 36

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<220>

<223> primer

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tttgaattct cacttgtcgt catcgtcttt gtagtctgca cttgcacatcgt tggtatcatg 60

<210> 11  
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<213> Artificial

<220>

<223> primer

<400> 11  
gacatctcct gtcccaag 18

<210> 12  
<211> 18  
<212> DNA  
<213> Artificial

<220>

<223> primer

<400> 12  
ctaacatgtt ctacatcg 18

<210> 13  
<211> 18

<212> DNA  
<213> Artificial

<220>  
<223> primer

<400> 13  
ctgtccacat cacagtcc

18

<210> 14  
<211> 19  
<212> DNA  
<213> Artificial

<220>  
<223> primer

<400> 14  
cagacagttcc ctgataaaag

19

<210> 15  
<211> 20  
<212> DNA  
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<220>  
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<400> 15  
ctcggttgc ttgcgttcac

20

<210> 16  
<211> 19  
<212> DNA  
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<220>  
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<400> 16  
gacttccaga ggcactggc

19

<210> 17  
<211> 19  
<212> DNA  
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<220>  
<223> primer

<400> 17  
ggctcctgtg gtggggtcg

19

<210> 18

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<220>  
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<400> 18  
ggttgcact gtcgatgg

18